Supplementary Information



Figure S1 – <sup>1</sup>H-NMR spectrum for compound **1** in DMSO-d<sup>6</sup>.



Figure S2 –  $^{13}$ C-NMR spectrum for compound **1** in DMSO-d<sup>6</sup>.



Figure S3 - <sup>1</sup>H-<sup>1</sup>H Selective ROESY (2.67 ppm, NH<sub>3</sub> signal) for compound **1** in DMSO-d<sup>6</sup>.



Figure S4 – Time-dependent <sup>1</sup>H-NMR spectroscopy for compound **1** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)) / DMSO (1:1).



Figure S5 – Time-dependent Diffusion Ordered Spectroscopy (DOSY) for compound **1** in  $D_2O/H_2O$  (1:9) after 0 Min (signal at -9.00 m<sup>2</sup>s<sup>-1</sup> was assigned to free DMSO added for solubility purposes).



Figure S6 – Time-dependent Diffusion Ordered Spectroscopy (DOSY) for compound **1** in  $D_2O/H_2O$  (1:9) after 24 h (signal at -9.00 m<sup>2</sup>s<sup>-1</sup> was assigned to free DMSO added for solubility purposes).



Figure S7 – Time-dependent Diffusion Ordered Spectroscopy (DOSY) for compound **1** in  $D_2O/H_2O$  (1:9) after 48 h (signal at -9.00 m<sup>2</sup>s<sup>-1</sup> was assigned to free DMSO added for solubility purposes).



Figure S8 – ESI(+) mass spectrum for compound **1**.





Figure S11 – Time-dependent <sup>1</sup>H-NMR spectroscopy for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S12 – Time-dependent Diffusion Ordered Spectroscopy (DOSY) after 0 Min for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S13 – Time-dependent Diffusion Ordered Spectroscopy (DOSY) after 24 h for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S14 – <sup>1</sup>H-<sup>1</sup>H Selective ROESY (1.36 ppm, CH<sub>3</sub> signal) after 0 Min for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S15 – <sup>1</sup>H-<sup>1</sup>H Selective ROESY (3.56 ppm, NH<sub>2</sub> signal) after 0 Min for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S16 – <sup>1</sup>H-<sup>1</sup>H Selective ROESY (1.36 ppm, CH<sub>3</sub> signal) after 24 h for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S17 – <sup>1</sup>H-<sup>1</sup>H Selective ROESY (2.50 ppm, free NH<sub>2</sub>Me) after 24 h for compound **2** in 1 M TRIS – 100 mM KCl (pH 7.2, prepared in  $D_2O/H_2O$  (1:9)).



Figure S18 – ESI(+) mass spectrum for compound 2.



Figure S19 – FID results for titration of 0.25  $\mu$ M *HTelo (K)* and 0.50  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S20 – FID results for titration of 0.25  $\mu$ M *HTelo (Na)* and 0.50  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S21 – FID results for titration of 0.25  $\mu$ M *c-myc* and 0.50  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S22 – FID results for titration of 0.25  $\mu$ M *c-kit2* and 0.50  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S23 – FID results for titration of 0.25  $\mu$ M *bcl2* and 0.50  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S24 – FID results for titration of 0.25  $\mu$ M *ds26* and 0.75  $\mu$ M TO with increasing amounts of complex **1** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S25 – FID results for titration of 0.25  $\mu$ M *c-myc* and 0.50  $\mu$ M TO with increasing amounts of complex **2** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S26 – FID results for titration of 0.25  $\mu$ M *ds26* and 0.75  $\mu$ M TO with increasing amounts of complex **2** (0 – 2.5  $\mu$ M): emission spectra (left) and %TO displacement (right). Titration was performed in 10 mM Licac + 100 mM KCl buffer (pH 7.2) at rt.



Figure S27 – DC<sub>50</sub> values for FID assays of complex  $\bf{1}$  and  $\bf{2}$  with different DNA sequences.



Figure S28 – FRET melting curves of different labelled DNA sequences in presence of complex **1**. Melting experiments were performed in triplicate. The mean is plotted above.



Figure S29 –  $\Delta T_m$  (°C) values for different DNA sequences are plotted in presence of increasing amounts of complex **1**. Results were obtained by averaging three independent experiments.

Table S1 –  $\Delta T_m$  (°C) values at a concentration of 1  $\mu$ M of complex **1** are listed for different DNA sequences. Triplicate experiments were used to calculate the standard deviation.

| DNA sequence | <b>ΔT</b> <sub>m</sub> (°C), 1 μΜ |
|--------------|-----------------------------------|
| HTelo (K)    | 16.8 ± 0.1                        |
| HTelo (Na)   | $4.5 \pm 0.3$                     |
| с-тус        | $20.0 \pm 0.2$                    |
| c-kit2       | $14.0 \pm 0.2$                    |
| bcl-2        | 8.7 ± 0.3                         |
| ds26         | 0.0 ± 0.1                         |
|              |                                   |



Figure S30 – FRET melting curves obtained for the competition assay are plotted above for a number of different DNA sequences in presence of complex **1**. Up to 600  $\mu$ M CT-DNA were added as competitor DNA. Details to conditions used for the experiments see Experimental Details. The mean is plotted for triplicate experiments.



Figure S31 – Molecular docking results for compound **1** with HTelo hybrid type (PDB: 2mb3, **A**) and HTelo basket type (PDB: 2mcc, **B**). The results were obtained using Autodock 4.2 and visualised with Chimera.

|          |       | B<br>S |       |       |       | やいろう  |         |   |
|----------|-------|--------|-------|-------|-------|-------|---------|---|
| Struct.  | 1     | 2      | 3     | 4     | 5     | 6     | Average | _ |
| 5W77 (A) | 1.658 | 1.805  | 2.130 | 2.514 | 2.790 | -     | 2.18    | _ |
| 2MCC (B) | 1.832 | 1.893  | 1.905 | 1.920 | 2.029 | 2.260 | 1.97    | _ |
| 2MB3 (C) | 1.717 | 2.028  | 2.038 | 2.292 | 2.614 | 2.788 | 2.25    | _ |
|          |       |        |       |       |       |       |         |   |

Figure S32 – Results from molecular docking studies showing the closest interactions between  $NH_3$  on compound **1** and guanine oxygens. Distances were measured in Chimera and  $NH\cdotsO$  distances above 3 Å were excluded. The PDB files listed are c-myc (5w77), HTelo basket type (2mcc) and HTelo hybrid type (2mb3).

|                 | ΔT <sub>m</sub> (°C) |               |                |               |            |  |
|-----------------|----------------------|---------------|----------------|---------------|------------|--|
| DNA<br>sequence | 0 µM                 | 0.6 µM        | 6.0 µM         | 60 µM         | 120 µM     |  |
| •               | CT-DNA               | CT-DNA        | CT-DNA         | CT-DNA        | CT-DNA     |  |
| HTelo (K)       | 17.4 ± 0.5           | 17.3 ± 0.7    | $17.0 \pm 0.4$ | 16.7 ± 0.5    | 17.0 ± 0.2 |  |
| HTelo (Na)      | 4.2 ± 0.5            | $3.5 \pm 0.4$ | $2.5 \pm 0.7$  | $2.6 \pm 0.7$ | 1.8 ± 0.6  |  |
| с-тус           | 23.5 ± 0.1           | 23.6 ± 0.3    | $23.3 \pm 0.4$ | 23.1 ± 0.1    | 23.0 ± 0.3 |  |
| c-kit2          | 13.4 ± 0.9           | 13.8 ± 1.0    | 13.5 ± 0.5     | 12.4 ± 0.7    | 11.8 ± 1.0 |  |
| bcl-2           | 7.4 ± 0.2            | 7.2 ± 0.8     | $6.6 \pm 0.6$  | 6.1 ± 0.7     | 5.9 ± 0.3  |  |

Table S2 – Overview of  $\Delta T_m$  (°C) values obtained for the FRET competition assay in presence of complex **1** and increasing amounts of CT DNA added to the sample. Three independent experiments were performed and results averaged to determine the standard deviation.